



1600

RAW SEQUENCE LISTING

DATE: 09/17/2004

PATENT APPLICATION: US/10/015,989A

TIME: 13:35:44

Input Set : A:\ORT1552 Seq Listing 9-2004.txt

Output Set: N:\CRF4\09172004\J015989A.raw

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3 <110> APPLICANT: Darrow, Andrew
4      Qi, Jenson
5      Andrade-Grodon, Patricia
7 <120> TITLE OF INVENTION: Zymogen Activation System
9 <130> FILE REFERENCE: ORT-1552
11 <140> CURRENT APPLICATION NUMBER: 10/015,989A
12 <141> CURRENT FILING DATE: 2001-12-10
14 <150> PRIOR APPLICATION NUMBER: 09/303,162
15 <151> PRIOR FILING DATE: 1999-04-30
17 <160> NUMBER OF SEQ ID NOS: 60
19 <170> SOFTWARE: PatentIn version 3.2
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 361
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Fusion Gene Vectors
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34 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctat      180
36 gctctagata gcggccgctt cccttttagtg agggttaatg cttcgagcag acatgataag      240
38 atacattgat gagtttggac aaaccacaac tagaatgcag tgaaaaaaat gctttatttg      300
40 tgaaatttgt gatgctattg ctttatttgt aaccattata agctgcaata aacaagttga      360
42 c                                                                                      361
45 <210> SEQ ID NO: 2
46 <211> LENGTH: 301
47 <212> TYPE: DNA
48 <213> ORGANISM: Artificial Sequence
50 <220> FEATURE:
51 <223> OTHER INFORMATION: Fusion Gene Vectors
53 <400> SEQUENCE: 2
54 gaattcacca tgaatccact cctgatacctt acctttgttg cggccgctct tgctgcccc      60
56 tttgatgatg atgacaagat cgttgggggc tattgtctag ataccctac gatgtgcccc      120
58 attacgccta gcggccgctt cccttttagtg agggttaatg cttcgagcag acatgataag      180
60 atacattgat gagtttggac aaaccacaac tagaatgcag tgaaaaaaat gctttatttg      240
62 tgaaatttgt gatgctattg ctttatttgt aaccattata agctgcaata aacaagttga      300
64 c                                                                                      301
67 <210> SEQ ID NO: 3
68 <211> LENGTH: 484
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:

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73 <223> OTHER INFORMATION: Fusion Gene Vector

75 <400> SEQUENCE: 3

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76 gaattcacca ccattggacag caaagggttcg tcgcagaaat cccgcctgct cctgctgctg      60
78 gtggtgtcaa atctactctt gtgccagggg gtggtctccg actacaagga cgacgacgac      120
80 gtggacgcgg ccgctcttgc tgcccccttt atcgaggggc gcattgtgga gggctcggat      180
82 ctagataccc ctacgatgtg cccgattacg ccgctagata cccctacgat gtgcccgat      240
84 acgcccgtag ataccactac gatgtgcccg attacgccgc tagatacccc tacgatgtgc      300
86 ccgattacgc ctacgcggccg ctccctctta gtgagggtta atgcttcgag cagacatgat      360
88 aagatacatt gatgagtttg gacaaaccac aactagaatg cagtgaaaaa aatgctttat      420
90 ttgtgaaatt tgtgatgcta ttgctttatt tgaaccatt ataagctgca ataaacaagt      480
92 tgac

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95 <210> SEQ ID NO: 4

96 <211> LENGTH: 382

97 <212> TYPE: DNA

98 <213> ORGANISM: Artificial Sequence

100 <220> FEATURE:

101 <223> OTHER INFORMATION: Fusion Gene Vectors

103 <400> SEQUENCE: 4

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106 gtggtgtcaa atctactctt gtgccagggg gtggtctccg actacaagga cgacgacgac      120
108 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctac      180
110 aactgtctag acatcaccat caccatcact agcggcgct tccctttagt gaggggtaat      240
112 gcttcgagca gacatgataa gatacattga tgagtttgga caaaccacaa ctagaatgca      300
114 gtgaaaaaaaa tgctttattt gtgaaatttg tgatgctatt gctttatttg taaccattat      360
116 aagctgcaat aaacaagttg ac

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119 <210> SEQ ID NO: 5

120 <211> LENGTH: 352

121 <212> TYPE: DNA

122 <213> ORGANISM: Artificial Sequence

124 <220> FEATURE:

125 <223> OTHER INFORMATION: Fusion Gene Vectors

127 <400> SEQUENCE: 5

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130 ttcggctgcg ggggtccccga ctacaaggac gacgacgacg cggccgctct tgctgcccc      120
132 tttgatgatg atgacaagat cgttgggggc tatgctctag acatcaccat caccatcact      180
134 agcggccgct tccctttagt gaggggtaat gcttcgagca gacatgataa gatacattga      240
136 tgagtttgga caaaccacaa ctagaatgca gtgaaaaaaaa tgctttattt gtgaaatttg      300
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141 <210> SEQ ID NO: 6

142 <211> LENGTH: 385

143 <212> TYPE: DNA

144 <213> ORGANISM: Artificial Sequence

146 <220> FEATURE:

147 <223> OTHER INFORMATION: Fusion Gene Vectors

149 <400> SEQUENCE: 6

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150 gaattcacca ccattggcttt cctctggctc ctctcctgct gggccctcct ggggtaccacc      60
152 ttcggctgcg ggggtccccga ctacaaggac gacgacgacg cggccgctct tgctgcccc      120
154 tttgatgatg atgacaagat cgttgggggc tatgctctag ataccctac gatgtgcccg      180
156 attacgccgc tagacatcac catcaccatc actageggcc gcttcccttt agtgagggtt      240

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158 aatgcttcga gcagacatga taagatacat tgatgagttt ggacaaacca caactagaat 300
160 gcagtgaataa aaatgcttta tttgtgaaat ttgtgatgct attgctttat ttgtaaccat 360
162 tataagctgc aataaacaag ttgac 385
165 <210> SEQ ID NO: 7
166 <211> LENGTH: 1169
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Fusion Gene With Homo Sapien Serine Protease Catalytic

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Domain

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173 <400> SEQUENCE: 7
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176 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga cgacgacgac 120
178 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctat 180
180 gctctagagg ccggtcagtg gccctggcag gtcagcatca cctatgaagg cgtccatgtg 240
182 tgtggtggct ctctcgtgtc tgagcagtggt gtgctgtcag ctgctcactg cttccccagc 300
184 gagcaccaca aggaagccta tgagggtcaag ctggggggccc accagctaga ctctactcc 360
186 gaggacgcca aggtcagcac cctgaaggac atcatcccc accccagcta cctccaggag 420
188 ggctcccagg gcgacattgc actcctccaa ctccagcagac ccatcacctt ctcccgtac 480
190 atccggccca tctgcctccc tgcagccaac gcctccttcc ccaacggcct ccaactgact 540
192 gtactgggtg ggggtcatgt ggccccctca gtgagcctcc tgacgcccga gccactgcag 600
194 caactcgagg tgcctctgat cagtcgtgag acgtgtaact gcctgtacaa catcgacgcc 660
196 aagcctgagg agccgcactt tgtccaagag gacatgggtg gtgctggcta tgtggagggg 720
198 ggcaaggacg cctgccaggg tgactctggg ggccccactc cctgccctgt ggagggtctc 780
200 tggtagctga cgggcattgt gagctgggga gatgcctgtg gggcccgcga caggcctggt 840
202 gtgtacactc tggcctccag ctatgcctcc tggatccaaa gcaagggtgac agaactccag 900
204 cctcgtgtgg tgccccaac ccaggagtcc cagcccgaca gcaacctctg tggcagccac 960
206 ctggccttca gctctagaca tcaccatcac catcactagc ggccgcttcc ctttagtgag 1020
208 ggtaaatgct tcgagcagac atgataagat acattgatga gtttggacaa accacaacta 1080
210 gaatgcagtg aaaaaaatgc tttatttgtg aaatttgtga tgctattgct ttatttgtaa 1140
212 ccattataag ctgcaataaa caagttgac 1169

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215 <210> SEQ ID NO: 8

216 <211> LENGTH: 1142

217 <212> TYPE: DNA

218 <213> ORGANISM: Artificial Sequence

220 <220> FEATURE:

221 <223> OTHER INFORMATION: Fusion Gene With Homo Sapien Serine Protease Catalytic

Domain

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226 ttcggctgcg ggggtcccca ctacaaggac gacgacgacg cggccgctct tgctgcccc 120
228 tttgatgatg atgacaagat cgttgggggc tatgctctag aggccggtca gtggccctgg 180
230 caggtcagca tcacctatga aggcgtccat gtgtgtggtg gctctctcgt gtctgagcag 240
232 tgggtgctgt cagctgctca ctgcttcccc agcgagcacc acaaggaagc ctatgaggtc 300
234 aagctggggg cccaccagct agactcctac tccgaggacg ccaagggtcag caccctgaag 360
236 gacatcatcc cccacccag ctacctccag gagggctccc agggcgacat tgcactcctc 420
238 caactcagca gacccatcac cttctccgcg tacatccggc ccatctgcct ccctgcagcc 480
240 aacgcctcct tccccaacgg cctccactgc actgtcactg gctgggggtca tgtggcccc 540
242 tcagttagcc tcctgacgcc caagccactg cagcaactcg aggtgcctct gatcagtcgt 600
244 gagacgtgta actgcctgta caacatcgac gccaaagcctg agggagccgca ctttgtccaa 660
246 gaggacatgg tgtgtgctgg ctatgtggag gggggcaagg acgcctgcc aagggtgactct 720

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248 ggggggcccac tctcctgccc tgtggagggt ctctggtacc tgacgggcat tgtgagctgg      780
250 ggagatgcct gtggggcccg caacaggcct ggtgtgtaca ctctggcctc cagctatgcc      840
252 tcttggatcc aaagcaaggt gacagaactc cagcctcgtg tgggtgcccc aaccaggag      900
254 tcccagcccg acagcaacct ctgtggcagc cacctggcct tcagctctag acatcaccat      960
256 caccatcact agcggccgct tccctttagt gagggttaat gcttcgagca gacatgataa     1020
258 gatacattga tgagtttgga caaaccacaa ctagaatgca gtgaaaaaaa tgctttatatt     1080
260 gtgaaatttg tgatgctatt gctttatttg taaccattat aagctgcaat aaacaagttg     1140
262 ac                                                                    1142

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265 <210> SEQ ID NO: 9

266 <211> LENGTH: 1049

267 <212> TYPE: DNA

268 <213> ORGANISM: Artificial Sequence

270 <220> FEATURE:

271 <223> OTHER INFORMATION: Fusion Gene With Homo Sapien Serine Protease Catalytic

Domain

273 <400> SEQUENCE: 9

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274 gaattcacca ccatggacag caaagggttcg tcgcagaaat cccgcctgct cctgctgctg      60
276 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga cgacgacgac     120
278 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctac     180
280 aactgtctag aacccattc gcagccttgg caggcggcct tgttccaggg ccagcaacta     240
282 ctctgtggcg gtgtccttgc aggtggcaac tgggtcctta cagctgcccc ctgtaaaaaa     300
284 ccgaaataca cagtacgcct gggagaccac agcctacaga ataaagatgg ccagagcaa     360
286 gaaatacctg tggttcagtc catcccacac ccctgctaca acagcagcga tgtggaggac     420
288 cacaaccatg atctgatgct tcttcaactg cgtgaccagg catccctggg gtccaaagtg     480
290 aagcccatca gcttggcaga tcattgcacc cagcctggcc agaagtgcac cgtctcaggc     540
292 tggggcactg tcaccagtcc ccgagagaat tttcctgaca ctctcaactg tgcagaagta     600
294 aaaatctttc ccagaagaa gtgtgaggat gcttaccggg ggcagatcac agatggcatg     660
296 gtctgtgcag gcagcagcaa aggggctgac acgtgccagg gcgattctgg agggccccctg     720
298 gtgtgtgatg gtgactcca gggcatcaca tcctggggct cagaccctg tgggagggtcc     780
300 gacaaacctg gcgtctatac caacatctgc cgctacctgg actggatcaa gaagatcata     840
302 ggcagcaagg gctctagaca tcaccatcac catcactagc ggccgcttcc ctttagtgag     900
304 ggtaaatgct tcgagcagac atgataagat acattgatga gtttggacaa accacaacta     960
306 gaatgcagtg aaaaaaatgc tttatttgtg aaatttgtga tgctattgct ttatttgtaa     1020
308 ccattataag ctgcaataaa caagttgac                                                                    1049

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312 <211> LENGTH: 1052

313 <212> TYPE: DNA

314 <213> ORGANISM: Artificial Sequence

316 <220> FEATURE:

317 <223> OTHER INFORMATION: Fusion Gene With Homo Sapien Serine Protease Catalytic

Domain

319 <400> SEQUENCE: 10

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322 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga cgacgacgac     120
324 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctac     180
326 aactgtctag aaaagcactc ccagccctgg caggcagccc tgttcgagaa gacgcggcta     240
328 ctctgtgggg cgacgctcat cgccccaga tggctcctga cagcagccca ctgcctcaag     300
330 ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg ctgtgagcag     360
332 acccggacag ccactgagtc cttccccccac cccggcttca acaacagcct ccccaacaaa     420
334 gaccaccgca atgacatcat gctggtgaag atggcatcgc cagtctccat cacctgggct     480
336 gtgcgacccc tcacctctc ctcacgctgt gtcactgctg gcaccagctg cctcatttcc     540

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338 ggctggggca gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
340 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat cacagacacc 660
342 atgggtgtgtg ccagcgtgca ggaagggggc aaggactcct gccaggggtga ctccgggggc 720
344 cctctggtct gtaaccagtc tcttcaaggc attatctcct ggggccagga tccgtgtgcg 780
346 atcacccgaa agcctgggtg ctacacgaaa gtctgcaa atgtggactg gatccaggag 840
348 acgatgaaga acaattctag acatcaccat caccatcact agcggccgct tccctttagt 900
350 gaggggttaat gcttcgagca gacatgataa gatacattga tgagtttgga caaaccacaa 960
352 ctagaatgca gtgaaaaaaa tgctttattt gtgaaatttg tgatgctatt gctttatttg 1020
354 taaccattat aagctgcaat aaacaagttg ac 1052

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358 <211> LENGTH: 328

359 <212> TYPE: PRT

360 <213> ORGANISM: Artificial Sequence

362 <220> FEATURE:

363 <223> OTHER INFORMATION: Fusion Gene With Homo Sapien Serine Protease Catalytic

Domain

365 <400> SEQUENCE: 11

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367 Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu Leu
368 1 5 10 15
371 Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
372 20 25 30
375 Asp Asp Asp Asp Val Asp Ala Ala Leu Ala Ala Pro Phe Asp Asp
376 35 40 45
379 Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Ala Gly Gln Trp Pro
380 50 55 60
383 Trp Gln Val Ser Ile Thr Tyr Glu Gly Val His Val Cys Gly Gly Ser
384 65 70 75 80
387 Leu Val Ser Glu Gln Trp Val Leu Ser Ala Ala His Cys Phe Pro Ser
388 85 90 95
391 Glu His His Lys Glu Ala Tyr Glu Val Lys Leu Gly Ala His Gln Leu
392 100 105 110
395 Asp Ser Tyr Ser Glu Asp Ala Lys Val Ser Thr Leu Lys Asp Ile Ile
396 115 120 125
399 Pro His Pro Ser Tyr Leu Gln Glu Gly Ser Gln Gly Asp Ile Ala Leu
400 130 135 140
403 Leu Gln Leu Ser Arg Pro Ile Thr Phe Ser Arg Tyr Ile Arg Pro Ile
404 145 150 155 160
407 Cys Leu Pro Ala Ala Asn Ala Ser Phe Pro Asn Gly Leu His Cys Thr
408 165 170 175
411 Val Thr Gly Trp Gly His Val Ala Pro Ser Val Ser Leu Leu Thr Pro
412 180 185 190
415 Lys Pro Leu Gln Gln Leu Glu Val Pro Leu Ile Ser Arg Glu Thr Cys
416 195 200 205
419 Asn Cys Leu Tyr Asn Ile Asp Ala Lys Pro Glu Glu Pro His Phe Val
420 210 215 220
423 Gln Glu Asp Met Val Cys Ala Gly Tyr Val Glu Gly Gly Lys Asp Ala
424 225 230 235 240
427 Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Cys Pro Val Glu Gly Leu
428 245 250 255
431 Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Asp Ala Cys Gly Ala Arg

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1

VERIFICATION SUMMARY

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